



Revised sequence listing.txt
SEQUENCE LISTING

<110> Stratagene
<120> HIGH FIDELITY DNA POLYMERASE COMPOSITIONS AND USES THEREFOR
<130> 25436/2155
<140> 10/079,241
<141> 2002-02-20
<160> 11
<170> PatentIn version 3.1

<210> 1
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved domain

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> Conserved domain, X at position 2 or 3 is any amino acid.

<400> 1

Asp Xaa Xaa Ser Leu Tyr Pro
1 5

<210> 2
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved domain

<220>
<221> MISC_FEATURE
<222> (2)..(7)
<223> Conserved domain, X at position 2, 3, 4, or 7 is any amino acid.

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Lys Xaa Xaa Xaa Asn Ser Xaa Tyr Gly
1 5

<210> 3
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved domain

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<220>
<221> misc_feature
<222> (2)..(3)
<223> Conserved domain, X at position 2 or 3 is any amino acid.

<400> 3

Thr Xaa Xaa Gly Arg
1 5

<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved domain

<220>
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<400> 4

Tyr Xaa Asp Thr Asp Ser
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<210> 5
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Conserved domain

<220>
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<222> (2)..(2)
<223> Conserved domain, X at position 2 is any amino acid.

<400> 5

Lys Xaa Tyr
1

<210> 6
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
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<221> MISC_FEATURE
<222> (2)..(2)

<223> Conserved domain, X at position 2 is any amino acid.

<400> 6

Tyr Xaa Gly Gly
1

<210> 7

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conserved domain

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<221> MISC_FEATURE

<222> (1)..(6)

<223> Conserved domain

<400> 7

Ser Tyr Thr Gly Gly Phe
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<210> 8

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic primer

<220>

<221> misc_feature

<222> (1)..(23)

<223> Synthetic primer

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23

<210> 9

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic primer

<220>

<221> misc_feature

<222> (1)..(23)

<223> Synthetic primer

<400> 9

gaggtacagg gttgaggcta ctg

23

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<210> 10
 <211> 776
 <212> PRT
 <213> Thermococcus sp. JDF-3

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Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
 20 25 30

Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
 35 40 45

Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
 50 55 60

Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
 65 70 75 80

Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
 85 90 95

Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
 145 150 155 160

Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile
 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys
 180 185 190

Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr
 195 200 205

Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu
 210 215 220

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Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys
 225 230 235 240
 Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val
 245 250 255
 His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
 260 265 270
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu
 275 280 285
 Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly
 290 295 300
 Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr
 305 310 315 320
 Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
 325 330 335
 Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
 340 345 350
 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
 355 360 365
 Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr
 370 375 380
 Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile
 385 390 395 400
 Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
 405 410 415
 Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp
 420 425 430
 Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
 435 440 445
 Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys
 450 455 460
 Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp
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Revised Sequence: 1st string.txt															
465				470				475				480			
Tyr	Arg	Gln	Arg	Ala 485	Ile	Lys	Ile	Leu	Ala 490	Asn	Ser	Tyr	Tyr	Gly 495	Tyr
Tyr	Gly	Tyr	Ala 500	Arg	Ala	Arg	Trp	Tyr 505	Cys	Arg	Glu	Cys	Ala 510	Glu	Ser
Val	Thr	Ala 515	Trp	Gly	Arg	Glu	Tyr 520	Ile	Glu	Met	Val	Ile 525	Arg	Glu	Leu
Glu	Glu 530	Lys	Phe	Gly	Phe	Lys 535	Val	Leu	Tyr	Ala	Asp 540	Thr	Asp	Gly	Leu
His 545	Ala	Thr	Ile	Pro	Gly 550	Ala	Asp	Ala	Glu	Thr 555	Val	Lys	Lys	Lys	Ala 560
Met	Glu	Phe	Leu	Asn 565	Tyr	Ile	Asn	Pro	Lys 570	Leu	Pro	Gly	Leu	Leu 575	Glu
Leu	Glu	Tyr	Glu 580	Gly	Phe	Tyr	Val	Arg 585	Gly	Phe	Phe	Val	Thr 590	Lys	Lys
Lys	Tyr	Ala 595	Val	Ile	Asp	Glu	Glu 600	Gly	Lys	Ile	Thr	Thr 605	Arg	Gly	Leu
Glu	Ile 610	Val	Arg	Arg	Asp	Trp 615	Ser	Glu	Ile	Ala	Lys 620	Glu	Thr	Gln	Ala
Arg 625	Val	Leu	Glu	Ala	Ile 630	Leu	Arg	His	Gly	Asp 635	Val	Glu	Glu	Ala	Val 640
Arg	Ile	Val	Arg	Glu 645	Val	Thr	Glu	Lys	Leu 650	Ser	Lys	Tyr	Glu	Val 655	Pro
Pro	Glu	Lys	Leu 660	Val	Ile	His	Glu	Gln 665	Ile	Thr	Arg	Glu	Leu 670	Lys	Asp
Tyr	Lys	Ala 675	Thr	Gly	Pro	His	Val 680	Ala	Ile	Ala	Lys	Arg 685	Leu	Ala	Ala
Arg	Gly 690	Val	Lys	Ile	Arg	Pro 695	Gly	Thr	Val	Ile	Ser 700	Tyr	Ile	Val	Leu
Lys 705	Gly	Ser	Gly	Arg	Ile 710	Gly	Asp	Arg	Ala	Ile 715	Pro	Phe	Asp	Glu	Phe 720

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Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln
725 730 735

Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
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Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp
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Leu Lys Pro Lys Gly Lys Lys Lys
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<210> 11
<211> 2331
<212> DNA
<213> Thermococcus sp. JDF-3

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